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LOCUS 1792251 369 bp mRNA EST 02-JUL-1999
DEFINITION FINT to contains Alu repetitive element; contains element MER4

ACCESSION AI792251

ACCESSION AI792251
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AUTHORS
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17
                                                                                                                                                                                               Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3187227.
Other_ESTs: np78b10.x5
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 369)
                                            NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                     Homo sapiens
                                                                                             human.
                                                                                                         AI792251.1 GI:5339967
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston L
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 Linehan, M.D., Rodrigo Chuaqui,
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AA61836 np30h03.s
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cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GCAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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putative full length read
The vector to vector length is
Seg primer: -40RP from Gibco.
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repetitive (
AI682287
AI682287.1
EST.
                                                                                                                A1682287 329 bp mRNA EST 26-MAY-1999 wC51c01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2322144 similar to contains alu repetitive element;contains element MEF
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/note-"Vector: pAMP10; Site_1): Not1; On 50 ng of
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
DNAse-treated, total cellular RNA obtained from
DNAse-treated, total cellular RNA obtained from
S,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors. 5 cycles of PCR applied to the
ligated to EcoRI adaptors. 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
DP. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

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                                                                                                 element ;, mRNA sequence.
                                       GI:4892469
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Homo sapiens

Ph.D

Sequencing Center information can be

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 375)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA)

Tumor Gene Index
Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1407086.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                    AA578209 375 bp mRNA EST 12-SEP-1997 m156f11.s1 NCI_CGAP_PF4 Homo sapiens cDNA clone IMAGE:1044717 similar to contains Alu repetitive element;contains element MER4 repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                         repetitive
AA578209
Email: Robert_Strausberg@nih.gov
T188ue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
".D., Michael R. Emmert-Buck, M.D., Ph.D.
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R02172 ye87e07.s1
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W45269 zc82e09.s1
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AA588 288 no25c12.s
AA714664 nx91h08.s
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AG012578 Homo sapi
AG012593 Homo sapi
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AG012594 Homo sapi
AG012594 Homo sapi
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                           Homo sapiens
Eukaryota; Metazoa; Cl
Eutheria; Primates; Cl
1 (bases 1 to 642)
Huang,G.M., Ng,W.l.,
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    Prostate cancer
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grade"
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                                  Farkas, J., He, L.,
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Pred. No. 4.8e-169;
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                                Liang, H.A., Gordon, D.,
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REFERENCE AUTHORS TITLE

09-AUG-1999

Yu,J.

JOURNAL COMMENT

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                      Unpublished (1997)
On Sep 12, 1996 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                 Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 375)
                                                                                                                                                        AA578209.1
EST.
                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                                                                                  Homo sapiens
                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                              Robert_Strausberg@nih.gov
                                                                                                                                                                  GI:2356393
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A1682251 np78b10.x
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A1792251 np78b10.x
AA631916 np78b10.s
AA631916 np30h03.s
AA618886 np30h03.s
AA618886 np30h03.s
AA618886 np30h03.x
AA618867 np30h03.x
AA618867 np30h03.x
AA60503931 RPCI-11-3
AA70503931 RPCI-11-3
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AQ313844 RPCI11-94

AQ563556 HS_5345A

AIG32528 wb10b03.x

AQ479186 RPCI-11-2

AW022746 df43al2.y
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AI467857 tj83g02.x
AQ346924 RPCI11-11
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H83957 ys64h05.s1
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AA197315 zq50f03.s
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315740 HS_5283_B
315758 HS_5230_B
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'67933 HS_3089_A

)620046 HS_5186_A

)77464 HS_2146_A

145997 HS_2226_A
     F. Chuaqui,
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182 CATCTACTTTGAAACATCTACTGG
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AI557474.1
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                                      Genomics 59 (2), 178-186 (1999) 9933-9982
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Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
           On Jun 5, 1998 this sequence version Contact: Guyang Matthew Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
Leroy Hood
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ang,G.M., Ng,W.1., Farkas,J.,
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/db_xref-"taxon:9606"
/clone-"IMAGE:1044717"
/clone-1ib-"NCI_CGAP_Pr4"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: prostate; Vector: pAMP10; mRNA made fi
prostate intraepithelial neoplasia (high-grade), cbl
made by oligo-dT priming. Non-directionally cloned
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/lab_host="DH10B"
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of Washington
of Molecular Biotechnology,
seattle, WA 98195

Box 357730, University

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AI792251
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Eukaryota; M
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unpublished (1997)
on Jun 5, 1998 this sequence version replaced g1:3187227
on Jun 5, 1998 this sequence version replaced g1:3187227
other_ESTs: np78b10.x5
Contact: Robert Strausberg, Ph.D.
rel: (301) 496-1550
                                                                                                            NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
                                                                                          Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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AA631916 np78b10.s
AA578209 nl56f11.s
A1557474 pr2.1_7_G
A1417931 tg55e07.x
AA876897 ny47g12.s
A1557019 pr2.1_10_
AA618586 np30h03.s
A1972706 wr42d04.x
A0503991 RpC17-11-3
A0503991 RpC17-11-3
A0503929 CIT-RSP-2
A0038229 CIT-RSP-2
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AA588288 no25c12.s

AA714684 nx91h08.s

AA503720 ne50f03.s

A1500579 tn93b04.x
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R01398 ye77a12.s1
W47326 zc39c12.r1
AA807307 oc38a01.s
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N70900 za33a05.s1
AQ586994 RPCI-11-4
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AI349788 ta96f08.x
AQ757670 HS_2274_B
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CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Sequencing Center

CDNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing NCI-CGAP clone distribution information can be

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGCGTGCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCCTGCTTGCA 62
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putative full length read
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Seq primer: -40RP from Gibco.
Location/Qualifiers
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nilarity 100.0%;
Conservative 0
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/dev_stage="45 years old"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAMp10; Site_1: Not1; Site_2: EcoRI; 1st
/note="Vector: pAMp10; Site_11: Not1; On 50 ng of
strand cDNA was primed with oligo(dT)17 on 50 ng of
strand cDNA was primed with oligo(dT)17 on 50 ng of
strand cDNA was primed with oligo(dT)17 on 50 ng of
strand cDNA was primed with operation intraepithelial
5,000-10,000 microdissected preneoplastic cells
5,000-10,000 microdissected preneoplastic cells
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histologically-determined to be prostatic intraepithelial
histologically-determined to be prostatic intraepithelial
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1,000-10,000 microdissale cells
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/db_xref="taxon:9606"
/clone="IMAGE:1132411"
/clone_lib="NCI_CGAP_Pr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
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Score 344; DB 60; ; pred. No. 2.5e-172; 0; Mismatches 0;

Length 369;

0

Gaps

0

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mRNA

26-MAY-1999

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5' data to verify this

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RESULT 1
AI792251
LOCUS
DEFINITION
                                                                                           REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
                                                                                                                                                                                          ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                  repetitive AI792251 AI792251.1 EST.
                                                                                                                                                                                                                           AI792251
np78bl0.y5
similar to
NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3187227.
Other_ESTs: np78b10.x5
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 369)
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 bp mRNA 02-JUL-1999 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411 contains Alu repetitive element;contains element ME element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                    GI:5339967
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N70900
AQ586994
T92000
AA702361
T96961
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AA455041
H73336
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AA503720
AI500579
W4152295
AI522295
R02172
W45269
R01398
W47326
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AA588288
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AI349788
AQ757670
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AI972706 wr42d04 x

AQ503931 RPCI-11-3

AQ566799 HS_2079_B

AQ038229 CIT-HSP-2

AG013338 Umm ----
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AQ012358 Homo sapi
AG012356 Homo sapi
AG012359 Homo sapi
AG012570 Homo sapi
AG012595 Homo sapi
AG012596 Homo sapi
AG012593 Homo sapi
AG012594 Homo sapi
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AA631916 np78b10.s
AA631917 pp72.1_7_6
A155731 tg55e07.x
AA876897 ny47g12.s
A1557019 PT2.1_10_
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A0586994 RPCI-11-4

T92000 ye01c12.s1

AA702361 z187902.s

T96961 ye50f08.s1
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AA620300 af05g04.s
AA455041 aa04a06.s
H73336 yu05d01.s1
AQ727006 HS_5431_A
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R045269 zc82e09.s1
R01398 ye77a12.s1
W47326 zc39c12.r1
AA807307 oc38a01.s
A1349788 ta96f08.x
AQ757670 HS_2274_B
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AA588288 no25c12.s

AA714684 nx91h08.s

AA503720 ne50f03.s

AI500579 tn93b04.x
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AA578209 n156f11.s
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AI522295 ti76e03.x
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Best Local Sim
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information
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cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington onlyersity Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The vector to vector length is seg primer: -40RP from Gibco.
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Putative full length read
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/note-"Vector: pAMP10; Site 1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
DNAse-treated, notoal sected preneoplastic cells
5,000-10,000 microdissected preneoplastic cells
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/lab_host-"DH10B"
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/clone_11b="NCI_CGAP_Pr2"
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/db_xref="taxon:9606"
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99.7%;
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Pred. No. 2e-145;
0; Mismatches 1;
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26-MAY-1999
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COMMENT
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KEYWORDS
SOURCE
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US-09-065-672-12 x T83743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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                                                                                                                                                                                                                                                      Align seg 1/1 to: T83743
                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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92
                                                                                                                     28 rThrLeuLysHisLeuLeuGlyGluThrArgSerAspGlySerAlaCysA 45
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                      snSerGlyIleSerGlyGlyArgGlyArgLysIle 56
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                                                                                CATCCIG..
                                                                                                                                                                  GCGCTACTGAGCAGTGATAAACAAAAGGTATTGAATAATGAAAAATCAAT
ATTNCAGCATTTTGGGAGGCCAAGGTAGGAGGATC 126
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1 (bases 1 to 387)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 742
                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 742
Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 258 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The washU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Eco RI sites of the modified pT7T3 vector. In went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

70 c 76 g 106 t 6 others
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71.111
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Gaps: 1
Percent Identity: 40.000
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                                                                                GCCAGGCACAGTGGCTCATGCTGTA
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seq_name: gb_est16:AA570478

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REFERENCE
AUTHORS
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ORGANISM
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US-09-065-672-12 x AA570478/rev
seq_name:
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LOCUS AA570478
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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                                                                                                                                                   177 CCCCTCTTTACTAAAAATACAAAAATTAGCCGGGCAT
                                                 136 CAGGCGCCTGTGATCCCAGCTACTCAGGAGGCCGAGGCAGAAGAATCCCT
                                                                                                                                                                                                                                                227 GGATCGCCTGAGGTCAGGAGTTCGAGATCAGCCTGGCTAACATGTCGAAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                          41 lySerAlaCysAsnSerGlyIleSerGlyGlyArgGlyArgLysIlePro 57
                                                                                                                                                                                          26 sThrSerThrLeuLys.....HisLeuLeuGlyGluThrArgSerAspG 41
                                                                                                                                                                                                                                                                            gb_gss14:AQ553229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40ml3 fwd. ET from High quality sequence stop: 440. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on May 8, 1995 this sequence version replaced gi:801198
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA570478 495 bp mRNA EST 25-AUG-1997 nk64a02.s1 NCI_CGAP_Schl Homo sapiens cDNA clone IMAGE:1018250 3'similar to contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: L. J
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA570478.1 GI:2344458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Organism="Homo sapiens"
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/tissue_type="Schwannoma tumor"
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/note="Vector: Bluescript SK; Site_1: EcoRI; Site_2:
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pooled bulk Schwannoma tumors. 5 adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.2 kb."
34 a 129 c 114 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.50
2.250
68.000
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Gaps:
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                                                                                                                                                   GGTG
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En<u>k</u>.
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                                                                                                                                                                                                                                                                                                                                                                                                 seg_name: gb_est4:R94063
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ORIGIN
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                                                                                                                                                                                                                                                                                                             DEFINITION
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US-09-065-672-13 x AA618586/rev
                                                                                                                                                                                                   OURCE
                                                                                                                                                                                                                                                ERSION
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Percent Similarity:/100.000
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       17 rLysSerAlaPheLeuSerAsnLysLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
                                                        Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 277)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                            R94063 277 bp mRNA EST 22-JAN-1999 Yt74a08.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE: 275991 3', mRNA sequence.
                                                                                                                                                                                                                                                                  R94063
                                                                                                                                                                                                                                        R94063.1 GI:969458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D./
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNY at:
www-bio.llnl.gov/bbrp/image/image.html
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397868
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 424 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to reverse of: AA618586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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/db_xref-"taxon:9606"
/clone="IMAGE:1117877"
/clone_lib-"NCI_CGAP_9f22"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-*Organ: profitate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal profitate bulk tissue, and was then primed with a Not I - ollfo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified gT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="normal prostate"
/lab_host="DH10B" /
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                                                                                                                                                                                                   Possic Accident
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: 100.000
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 Michael R.
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ACCESSION
VERSION
                                                SOURCE
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                                                                                                                             seq_documentation_block: LOCUS N74923
                                                                                                                                                               seq_name: gb_est6:N74923
                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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                                     ORGANISM
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                                                                                                                                                                                            79
                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                       29 CATTTTACAGAAAGGGAACCATAACATTACACAACAAAGTNTAGCTGTAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                        5 HisPheSerAspGlnGlyProAlaHisLeuThrThrSerLysSerAlaPh
                                                                                                                                                                                           AATCTCAAATAAGAAA
                                                                                                                                                                                                                  eLeuSerAsnLysLys 26
                                                                                           N74923 261 bp mRNA EST 29-MAR-1996
za45d03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
IMAGE:295493 3', mRNA sequence.
                                   Homo sapiens
                                                                          N74923
N74923.1 GI:1237469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
On Apr 14, 1993 this sequence version replaced
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
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The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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3.412
77.273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares fetal liver spleen lNFLS"
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                                                                                                                                                                                                                                                                                                                                                          Length: 22
Gaps: 0
Percent Identity: 50.000
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1026-1-5-1996
1026-1
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ORGANISM

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REFERENCE
AUTHORS
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ORIGIN
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                                                                       SOURCE
ORGANISM
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LOCUS AA280704
                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est12:AA280704
                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                               KEYWORDS
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JOURNAL
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09-065-672-13 x N74923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCTCAAATAAGAAA 103
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Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: ml3 -40 forward
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On May 18, 1995 th
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Hillier,L., Clark.N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                        zs96g03.s1 NCI_CGAP_GCB1 Homo sapiens mRNA sequence.
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                                                                           Homo sapiens
                                                                                                                                                                                    AA280704.1 GI:1923401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev stage="20 week-post conception fetus"
//dev stage="20 week-post conception fetus"
//lab_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: Library
//note="Organ: Library and Eco RI sites of the modified pT73 vector: Library
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/clone="IMAGE:295493"
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/db_xref-"GDB:1240414"
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102(N)
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251 CATTTTACAGAAAGGGAACCATAACATTACACAAAGTATAGCTGTAA 202
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1 (bases 1 to 306)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394868.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham.
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                                                                                                                                                                                       239296 331 bp mRNA EST 31-OCT-1994 HSC16F052 normalized infant brain cDNA Homo sapiens cDNA clone
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1 (bases 1 to 331)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                  Homo sapiens
                                                                                                                                                                         c-16f05 3', mRNA sequence.
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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/clone_1ib="NCI_CGAP_GCB1"
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US-09-065-672-13 x 239296
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LOCUS AI023420
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
                                                                                                                                                                                                                                                               0471g05.xl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1652312 3', mRNA sequence.
                                                                                               Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.

[ (bases 1 to 340)
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AI023420.1 GI:3239826
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Single read. 22 T removed at sequence 5'end
Genexpress_library_ldt: C; Genexpress_sequence_idt: alc-16f05
Seq primer: (-21)M13_universal.
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1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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IMAGE: molecular integration of the analysis of the human genome
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/dev_stage="3 months old"
/note="organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="notI; sex-Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5', '3' into the HindIII; NotI sites of the
cloned 5', '3' into the HindIII are not sex prophiatry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dept. Columbia University, USA.
Bento Soares, P.N.A.S in press*
61 c 47 g 91 t
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/sex="Female"
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/db_xref="taxon:9606"
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102 AATCTCAAATAAGAAA 117
                                21 eLeuSerAsnLysLys 26
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                                                              CATTTTACAGAAAGGGAACCATAACATTACACAACAAAGTATAGCTGTAA 101
                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 9, 1998 this sequence version replaced gi:937906.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 911 Std Error: 0.00
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High quality sequence stop: 332.
Location/Qualifiers
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60 c 48 g 102 t
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77.273
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-09-065-672-14 x C26462
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t Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
N80180
N80180.1 GI:1242881
EST.
                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 157.
Location/Qualifiers
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1 (bases 1 to 334)

Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                 The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785498.
Contact: Wilson RK
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Fax: 0298-38-7468
Email: tsasaki@ab
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/de_stage="callus"
74 c 174 g 56 t
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/db_xref="GDB:1242390"
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alignment_block:
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121 CAGCTACTCAGGAGGCAGGAGAA 94
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               18 rGlyIleSerGlyGlyArgGlyArgLys 27
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Gaps: 1
Percent Identity: 57.692
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                                     Unpublished (1997)
On Sep 12, 1996 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausherganic
                                                                                                                                                                                                                                                                                                                                              #A578209 ... 375 bp mRNA EST 12-SEP-1997 in156f11.sl NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1044717 similar to contains Alu repetitive element;contains element ME repetitive element; mRNA sequence.

A578209 ... MRNA sequence.
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D.,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates;
1 (bases 1 to 375)
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EST.
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AA918586 np30h03.s
A1972706 wf42404.x
AQ503931 RPCI-11-3
AQ560799 HS_2079_B
AQ038229 CIT-HSP-2
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H73336 yu05401.sl

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AQ586994 RPCI-11-4

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AA702361 z187g02.s
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AA714684 nx91h08.s

AA503720 ne50f03.s

AI500579 tn93b04.x

W47327 zc39c12.s1

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                             Rodrigo F. Chuaqui
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Homo sapiens
Eukaryota; Metazoa; Cl
Eutheria; Primates; Ct
1 (bases 1 to 642)
Huang,G.M., Ng,W.1., 1
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Seq primer: -40ml3
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ilarity 100.0%;
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/db_xref="taxon:9606"
/clone="IMAGE:1044717"
/clone_lib="NCI_CGAP_Pr4"
/sex="male"
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Location/Qualifiers
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     Farkas,J., He,L.,
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i; Hominidae; Homo.
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LOCUS AA631916 1025 380 bp mRNA
DEFINITION np78b10.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411
similar to contains Alu repetitive element;contains element MER4
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US-09-065-672-12 x AA876897
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Ratio: 5.228
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ame:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GlyArgGlyArgLysIlePro 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ATGTTGTGCGCCCATTTCTCAGATCAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCGAGGCAGGAAGATTCCT 290
                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est17:AA631916
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 380)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
On Sep 12, 1996 this sequence version replaced gi:1406914 Contact: Robert Strausberg, Ph.D.
                                                          Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                              repetitive element ;, mRNA sequence
AA631916
                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                          AA631916.1 GI:2554527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pAMP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1274950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Pr12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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6
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                                                                                    Anatomy Project (CGAP),
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seq_documentation_block:
                                                                                                                                                           seq_name:
                      VERSION
                                            DEFINITION
ACCESSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-065-672-12 x AA631916/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 298.00
Ratio: 5.228
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                             164 TGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAATTCTGGAATTTCGGGA
                                                                                                                                                                                                                                                                                                                                                                                        214 CAAGAGTGCTTTTCTCTCTAATAAGAAAACATCTACTTTGAAACATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC
                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                      17 rLysSerAlaPheLeuSerAsnLysLysThrSerThrLeuLysHisLeuL 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe
                                                                                                                                                                                                                                       GlyArgGlyArgLysIlePro 57
                                                                                                                                                                                                       GGCCGAGGCAGGAAGATTCCT
                                                                                                                                                           gb_est29:AI557474
                                         AI557474 642 bp mRNA EST PT2.1_7_G02.r tumor2 Homo sapiens cDNA 3', r AI557474
EST.
                   AI557474.1 GI:4489837
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CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnl.gov/bbrp/image/image.html
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="45 years old"
/lab_host="pH10B"
/lab_host="pH10B"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
strand_cDNA was primed with oligo(dT)17 on 50 ng of
DNAse=treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
pCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1132411"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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Gaps: 0
Percent Identity: 100.000
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d. ET from Amersham.
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                                                        mRNA sequence
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                                                                            09-AUG-1999
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SOURCE

ORGANISM

Homo sapiens

11:52:25

Percent Similarity: 100.000

Percent Identity: 100.000

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 rLysSerAlaPheLeuSerAsnLysLysThrSer 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1135022.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 370)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wr42d04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2490343 3'
similar to contains Alu repetitive element;contains element MER4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Michael J. Brownstein, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert_Strausberg@nih.gov
                                                                                                                    /note-"organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_PT22 was prepared, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2490343"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Pr28"
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alignment_scores:
Quality:
Ratio:
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alignment_scores:

Quality:

146.00

Length:

28

146.00 5.214

Length: Gaps:

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AUTHORS
TITLE
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US-09-065-672-13 x AI972706/rev
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1407086
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: W. Marston Line, Ph.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, No.D., Rodrigo F. Chuaqui, C.DNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 primer:
                        110
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                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1044717"
/clone_lib="NCI_CGAP_Pr4"
/sex="male"
                        þ
                                                                                    /note-"Organ: prostate; Vector: pamp10; mRNA made from prostate intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally close made by oligo-dT priming.
                                                                                                                                                                                                                  /tissue_type="prostatic intraepithelial neoplasia -grade"
                                                                     Size-selected
                                                                                                                                                                /dev_stage="adult"
/lab_host="DH10B"
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                                                                       on agarose gel,
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                                                                          average insert size 600 bp
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VERSION
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LOCUS AA876897
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US-09-065-672-13 x AA578209
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                                                                       Quality: 146.00
Ratio: 5.214
ent Similarity: 100.000
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High quality sequence stop: 376.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNE at:
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On Feb 13, 1998 this sequence version replaced gi:2761085.
Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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13 x AA876897
                                                                                                                                                                                                                                                                                          /note="Vector: pamp10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. won-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1274950"
                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Pr12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406914.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Seg primer: -40ml3 fwd.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1132411"
                                                                                                                                                                                                                                                                                                                             /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                       /sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Quality: Ratio:

146.00 5.214

Length:

seq_name: gb_est34:AI792251

17 nSerGlyIleSerGlyGlyArgGlyArgLys 27 TTCTGGAATTTCGGGAGGCCGAGGCAGGAAG

89

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BASE COUNT
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Tissue Procurement: W. Marston, h.D., Ph.D.
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found, through the I.M.A.G.E. Consortium/LLNL at:
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Contact: Robert Strausherg Dr D
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: -40RP from Gibco.
Location/Qualifiers
//dev_stage="45 years old"
//dev_stage="45 years old"
//lab_host="pHD10B"
//note="Vector: pAMP10; Site_1: Not1::Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ct: Robert Strausberg, Ph.D.
(301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resequenced clone has no previous 5' data to verify this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1132411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Pr2"
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alignment_scores:

Quality:

141.00

Length:

27

alignment_scores:

Quality: Ratio:

141.00 5.222

Length:

0

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est16:AA578209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThrLeuLysHisLeuLeuGlyGluThrArgSerAspGlySerAlaCysAs
                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: W. Marston Linehan, M.D., Rodr M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution i found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onpublished (1997)
on sep 12, 1996 this sequence version replaced gi:1407086
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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1 (bases 1 to 375)
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                           110 a
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                                                                                          /note-"Organ: prostate; Vector: pAMP10; mRNA made from prostate intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned
                                                                       Size-selected
                                                                                                                                                                  /dev_stage="adult"
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/clone_lib="NCI_CGAP_Pr4"
                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                    'tissue_type="prostatic intraepithelial neoplasia - high
                                                                                                                                                                                                                                                          'sex="male"
                        87 c
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                                                                    on agarose gel, average insert size 600 bp.
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88
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    Quality:
    Ratio:
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US-09-065-672-14 x AA578209
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                                                         Quality: 141.00
Ratio: 5.222
Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB/6897 378 bp mRNA EST 25-MAR-1998 ny47912.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1274950 similar to contains Alu repetitive element:contains element LTR3 AA876897 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Feb 13, 1998 this sequence version replaced g1:2761085 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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x AA876897
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                                                                                                                                                                                                                                          Non-directionally cloned. s average insert size 600 bp. NIH."
                                                                                                                                                                                                                                                   /note-"Vector: pAMP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman,
                                                                                                                                                                                                                                                                                                                                                      /tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1274950"
/clone_lib="NCI_CGAP_Pr12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                    /sex≖"male"
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                                                       Length: 27
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index

Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406914.
Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 380)
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                              87
/note="Vector: pAMP10; Site_1: Not1; Site_2: ECORI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to ECORI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1132411"
                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Pr2"
/sex="Male"
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alignment_scores:

Quality: Ratio:

141.00 5.222